

SEQUENCE LISTING

<110> NIIGATA TLO CORPORATION

<120> Vector for gene therapy and method for quantifying target protein in mammal or cultured cell to which the vector for gene therapy was administered

<130> 03PF275-PCT

<150> JP 2003-3967

<151> 2003-01-10

<160> 24

<210> 1

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> oligopeptide encoding C19-29 region of glucagon of human, mouse or rat

<400> 1

Ala Gln Asp Phe Val Gln Trp Leu Met Asn Thr

1

5

10

<210> 2

<211> 1471

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (13).. (1461)

<223> DNA insert encoding rat IFN- γ receptor, rat IgG Fc region and glucagon C19-29 region

<400> 2

gaattcattt aa atg att ctg ctg gtg gtc ctg atg ctg tct gcg gag atc 51

Met Ile Leu Leu Val Val Leu Met Leu Ser Ala Glu Ile

1

5

10

ggg agt gga gct ttg atg agc acc gag gat cct aag ccg ccc tcg gtg 99

Gly Ser Gly Ala Leu Met Ser Thr Glu Asp Pro Lys Pro Pro Ser Val

15

20

25

cct gcg cca aca aat gtt cta att acg tcc tat gac ttg aac cct gtc 147

Pro Ala Pro Thr Asn Val Leu Ile Thr Ser Tyr Asp Leu Asn Pro Val

30

35

40

45

gta cat tgg aag cac cag aac gtg tcg cag gct gcc gtc ttc act gta 195

Val His Trp Lys His Gln Asn Val Ser Gln Ala Ala Val Phe Thr Val

50

55

60

cag gta aag atg tat cca gaa tac tgg act gat gcc tgc acc aac att 243

Gln Val Lys Met Tyr Pro Glu Tyr Trp Thr Asp Ala Cys Thr Asn Ile

65

70

75

gcc cat cat tat tgt aat atc tac aaa cac att tcc tat cct gac tca 291

Ala His His Tyr Cys Asn Ile Tyr Lys His Ile Ser Tyr Pro Asp Ser

80

85

90

tct gcc tgg gcc aga gtt aag gcc aag gtt gga caa aga gaa tct gcc 339

Ser Ala Trp Ala Arg Val Lys Ala Lys Val Gly Gln Arg Glu Ser Ala

95

100

105

tat gog cag tca gaa gag ttt att atg tgc cga aag ggg aag gtt gga 387

Tyr Ala Gln Ser Glu Glu Phe Ile Met Cys Arg Lys Gly Lys Val Gly

110

115

120

125

ccg cct ggc ctg gac atc gga agg aag gaa gat cag ctg att gtc cac 435

Pro Pro Gly Leu Asp Ile Gly Arg Lys Glu Asp Gln Leu Ile Val His

130	135	140	
ata ttt cac cct aag gtc aat gtg agt cag gaa acc atg ttt ggt gac			483
Ile Phe His Pro Lys Val Asn Val Ser Gln Glu Thr Met Phe Gly Asp			
145	150	155	
gga aat acc tgt tac aca ttc gac tac act gtg ttt gtg aaa cat tac			531
Gly Asn Thr Cys Tyr Thr Phe Asp Tyr Thr Val Phe Val Lys His Tyr			
160	165	170	
agg agt ggg gag atc cta cat aca gaa cat agc gtc cta aaa gaa gat			579
Arg Ser Gly Glu Ile Leu His Thr Glu His Ser Val Leu Lys Glu Asp			
175	180	185	
tgt agc gaa act ctg tgt gag tta aac atc tca gtg tcc acg ctg aat			627
Cys Ser Glu Thr Leu Cys Glu Leu Asn Ile Ser Val Ser Thr Leu Asn			
190	195	200	205
tcc aat tac tgt gtt tca gta gtt gga aag tcg tct ttc tgg caa gtt			675
Ser Asn Tyr Cys Val Ser Val Val Gly Lys Ser Ser Phe Trp Gln Val			
210	215	220	
aat aca gaa aca tca aaa gac gcc tgt atc ccc ttt ctc cat gat gac			723
Asn Thr Glu Thr Ser Lys Asp Ala Cys Ile Pro Phe Leu His Asp Asp			
225	230	235	
aga gaa gaa gcg gcc gcc gtg ccc aga aac tgt gga ggt gat tgc aag			771
Arg Glu Glu Ala Ala Ala Val Pro Arg Asn Cys Gly Gly Asp Cys Lys			
240	245	250	
cct tgt ata tgt aca ggc tca gaa gta tca tct gtc ttc atc ttc ccc			819
Pro Cys Ile Cys Thr Gly Ser Glu Val Ser Ser Val Phe Ile Phe Pro			
255	260	265	
cca aag ccc aaa gat gtg ctc acc atc act ctg act cct aag gtc acg			867
Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val Thr			

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270	275	280	285	
tgt gtt gtg gta gac att agc cag gac gat ccc gag gtc cat ttc agc				915
Cys Val Val Val Asp Ile Ser Gln Asp Asp Pro Glu Val His Phe Ser				
290	295	300		
tgg ttt gta gat gac gtg gaa gtc cac aca gct cag act cga cca cca				963
Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Arg Pro Pro				
305	310	315		
gag gag cag ttc aac agc act ttc cgc tca gtc agt gaa ctc ccc atc				1011
Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro Ile				
320	325	330		
ctg cac cag gac tgg ctc aat ggc agg acg ttc aga tgc aag gtc acc				1059
Leu His Gln Asp Trp Leu Asn Gly Arg Thr Phe Arg Cys Lys Val Thr				
335	340	345		
agt gca gct ttc cca tcc ccc atc gag aaa acc atc tcc aaa ccc gaa				1107
Ser Ala Ala Phe Pro Ser Pro Ile Glu Lys Thr Ile Ser Lys Pro Glu				
350	355	360	365	
ggc aga aca caa gtt ccg cat gta tac acc atg tca cct acc aag gaa				1155
Gly Arg Thr Gln Val Pro His Val Tyr Thr Met Ser Pro Thr Lys Glu				
370	375	380		
gag atg acc cag aat gaa gtc agt atc acc tgc atg gta aaa ggc ttc				1203
Glu Met Thr Gln Asn Glu Val Ser Ile Thr Cys Met Val Lys Gly Phe				
385	390	395		
tat ccc cca gac att tat gtg gag tgg cag atg aac ggg cag cca cag				1251
Tyr Pro Pro Asp Ile Tyr Val Glu Trp Gln Met Asn Gly Gln Pro Gln				
400	405	410		
gaa aac tac aag aac act cca cct acg atg gac aca gat ggg agt tac				1299
Glu Asn Tyr Lys Asn Thr Pro Pro Thr Met Asp Thr Asp Gly Ser Tyr				

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415	420	425	
ttc ctc tac agc aag ctc aat gtg aag aag gaa aaa tgg cag cag gga			1347
Phe Leu Tyr Ser Lys Leu Asn Val Lys Lys Glu Lys Trp Gln Gln Gly			
430	435	440	445
aac acg ttc acg tgt tct gtg ctg cat gaa ggc ctg cac aac cac cat			1395
Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn His His			
	450	455	460
act gag aag agt ctc tcc cac tct ccg ggt aaa gcc caa gat ttt gtg			1443
Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys Ala Gln Asp Phe Val			
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cag tgg ttg atg aat acc tgagaattct			1471
Gln Trp Leu Met Asn Thr			
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<210> 3

<211> 4790

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA sequence of artificial expression vector pCAGGS

<400> 3

gtcgacattg attattgact agttattaat agtaatcaat tacgggggtca ttagttcata 60

gcccatatat ggagttccgc gttacataac ttacggtaaa tggcccgctt ggctgaccgc 120

ccaacgaccc cggcccattg acgtcaataa tgacgtatgt tccatagta acgccaatag 180

ggactttcca ttgacgtcaa tgggtggact atttacgta aactgcccac ttggcagtac 240

atcaagtgtg tcatatgccg agtacgcccc ctattgacgt caatgacggt aaatggcccc 300

cctggcatta tgcccagtac atgacottat gggactttcc tacttggcag tacatctacg 360
 tattagtcat cgctattacc atgggtcgag gtgagcccca cgttctgctt cactctcccc 420
 atctcccccc cctccccacc cccaattttg tatttattta ttttttaatt attttgtgca 480
 gcgatggggg cggggggggg gggggcgcg cccaggcggg gcggggcggg gcgaggggcg 540
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gatccgcac	tcaattagtc	agcaaccata	gtcccgcccc	taactccgcc	catcccgccc	2520
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gacagtatit	ggtatctgcg	ctctgctgaa	gccagttacc	ttcggaaaaa	gagttggtag	3540

ctcttgatcc ggcaaacaaa ccaccgctgg tagcgggtgt ttttttgtt gcaagcagca 3600
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 tatgcggcga ccgagttgct ctgcccggc gtcaatacgg gataataccg cgccacatag 4440
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 cttaccgctg ttgagatcca gttcgatgta acccactcgt gcaccaact gatcttcagc 4560
 atcttttact ttcaccagcg tttctgggtg agcaaaaaca ggaaggcaaa atgccgcaaa 4620

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aaaggaata agggcgacac ggaaatgttg aataactcata ctotctcttt ttcaatatta 4680
ttgaagcatt tatcagggtt attgtotcat gagcggatac atatttgaat gtatttagaa 4740
aaataaaca ataggggttc cgcgcacatt tccccgaaaa gtgccacctg 4790

<210> 4

<211> 1233

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (13).. (1224)

<223> DNA insert encoding rat CTLA4, rat IgG Fc region and glucagon C19-29 region

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Met Ala Cys Leu Gly Leu Gln Arg Tyr Lys Thr His Leu
1 5 10

cag ctg cct tct agg act tgg cct ttt gga gtc ctg ctt tct ctt ctc 99
Gln Leu Pro Ser Arg Thr Trp Pro Phe Gly Val Leu Leu Ser Leu Leu
15 20 25

ttc atc cca atc ttc tct gaa gcc ata caa gtg acc caa cct tca gtg 147
Phe Ile Pro Ile Phe Ser Glu Ala Ile Gln Val Thr Gln Pro Ser Val
30 35 40 45

gtg ttg gcc agc agc cac ggt gtc gcc agc ttt cca tgt gaa tat gca 195
Val Leu Ala Ser Ser His Gly Val Ala Ser Phe Pro Cys Glu Tyr Ala
50 55 60

tct tca cac aac act gat gag gtc cgg gtg acg gtg ctg cgg cag aca 243
Ser Ser His Asn Thr Asp Glu Val Arg Val Thr Val Leu Arg Gln Thr

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65	70	75	
aat gac caa gtg aca gag gtc tgt gcc acg aca ttc aca gtg aag aac			291
Asn Asp Gln Val Thr Glu Val Cys Ala Thr Thr Phe Thr Val Lys Asn			
80	85	90	
acg ttg ggc ttc cta gat gac ccc ttc tgc agt ggt acc ttt aat gaa			339
Thr Leu Gly Phe Leu Asp Asp Pro Phe Cys Ser Gly Thr Phe Asn Glu			
95	100	105	
agc aga gtg aac ctc acc atc caa gga ctg agg gct gct gac acc gga			387
Ser Arg Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Ala Asp Thr Gly			
110	115	120	125
ctg tac ttc tgc aag gtg gaa ctc atg tac cca ccg cca tac ttt gtg			435
Leu Tyr Phe Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Phe Val			
130	135	140	
ggc atg ggc aac ggg acc cag att tat gtc atc gat cca gaa cca tgc			483
Gly Met Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys			
145	150	155	
cca gat tca gac gcg gcc gcc gtg ccc aga aac tgt gga ggt gat tgc			531
Pro Asp Ser Asp Ala Ala Ala Val Pro Arg Asn Cys Gly Gly Asp Cys			
160	165	170	
aag cct tgt ata tgt aca ggc tca gaa gta tca tct gtc ttc atc ttc			579
Lys Pro Cys Ile Cys Thr Gly Ser Glu Val Ser Ser Val Phe Ile Phe			
175	180	185	
ccc cca aag ccc aaa gat gtg ctc acc atc act ctg act cct aag gtc			627
Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val			
190	195	200	205
acg tgt gtt gtg gta gac att agc cag gac gat ccc gag gtc cat ttc			675
Thr Cys Val Val Val Asp Ile Ser Gln Asp Asp Pro Glu Val His Phe			

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210	215	220	
agc tgg ttt gta gat gac gtg gaa gtc cac aca gct cag act cga cca			723
Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Arg Pro			
225	230	235	
cca gag gag cag ttc aac agc act ttc cgc tca gtc agt gaa ctc ccc			771
Pro Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro			
240	245	250	
atc ctg cac cag gac tgg ctc aat ggc agg acg ttc aga tgc aag gtc			819
Ile Leu His Gln Asp Trp Leu Asn Gly Arg Thr Phe Arg Cys Lys Val			
255	260	265	
acc agt gca gct ttc cca tcc ccc atc gag aaa acc atc tcc aaa ccc			867
Thr Ser Ala Ala Phe Pro Ser Pro Ile Glu Lys Thr Ile Ser Lys Pro			
270	275	280	285
gaa ggc aga aca caa gtt cgc cat gta tac acc atg tca cct acc aag			915
Glu Gly Arg Thr Gln Val Pro His Val Tyr Thr Met Ser Pro Thr Lys			
290	295	300	
gaa gag atg acc cag aat gaa gtc agt atc acc tgc atg gta aaa ggc			963
Glu Glu Met Thr Gln Asn Glu Val Ser Ile Thr Cys Met Val Lys Gly			
305	310	315	
ttc tat ccc cca gac att tat gtg gag tgg cag atg aac ggg cag cca			1011
Phe Tyr Pro Pro Asp Ile Tyr Val Glu Trp Gln Met Asn Gly Gln Pro			
320	325	330	
cag gaa aac tac aag aac act cca cct acg atg gac aca gat ggg agt			1059
Gln Glu Asn Tyr Lys Asn Thr Pro Pro Thr Met Asp Thr Asp Gly Ser			
335	340	345	
tac ttc ctc tac agc aag ctc aat gtg aag aag gaa aaa tgg cag cag			1107
Tyr Phe Leu Tyr Ser Lys Leu Asn Val Lys Lys Glu Lys Trp Gln Gln			

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350	355	360	365	
gga aac acg ttc acg tgt tct gtg ctg cat gaa ggc ctg cac aac cac				1155
Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn His				
	370	375	380	

cat act gag aag agt ctc tcc cac tct ccg ggt aaa gcc caa gat ttt				1203
His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys Ala Gln Asp Phe				
	385	390	395	

gtg cag tgg ttg atg aat acc tgagaattc				1233
Val Gln Trp Leu Met Asn Thr				
	400			

<210> 5

<211> 1143

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (13)..(1134)

<223> DNA insert encoding rat IL13, rat IgG Fc region and glucagon C19-29 region

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gaattcattt aa atg gca ctc tgg gtg act gca gtc ctg gct ctc gct tgc	51
Met Ala Leu Trp Val Thr Ala Val Leu Ala Leu Ala Cys	
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ctt ggt ggt ctt gcc acc cca ggg cca gtg cgg aga tcc aca tct ccc	99
Leu Gly Gly Leu Ala Thr Pro Gly Pro Val Arg Arg Ser Thr Ser Pro	
15 20 25	

cct gtg gcc ctc agg gag ctt atc gag gag ctg agc aac atc aca caa	147
Pro Val Ala Leu Arg Glu Leu Ile Glu Glu Leu Ser Asn Ile Thr Gln	
30 35 40 45	

gac cag aag act tcc ctg tgc aac agc agc atg gta tgg agc gtg gac	195
Asp Gln Lys Thr Ser Leu Cys Asn Ser Ser Met Val Trp Ser Val Asp	
50 55 60	
ctg aca gct ggc ggg ttc tgt gca gcc ctg gaa tcc ctg acc aac atc	243
Leu Thr Ala Gly Gly Phe Cys Ala Ala Leu Glu Ser Leu Thr Asn Ile	
65 70 75	
tcc agt tgc aat gcc atc cac agg acc cag agg ata ttg aat ggc ctc	291
Ser Ser Cys Asn Ala Ile His Arg Thr Gln Arg Ile Leu Asn Gly Leu	
80 85 90	
tgt aac caa aag gcc tcg gat gtg gct tcc agc ccc cca gat acc aaa	339
Cys Asn Gln Lys Ala Ser Asp Val Ala Ser Ser Pro Pro Asp Thr Lys	
95 100 105	
atc gaa gta gcc cag ttt ata tca aaa ctg ctc aat tac tcc aag caa	387
Ile Glu Val Ala Gln Phe Ile Ser Lys Leu Leu Asn Tyr Ser Lys Gln	
110 115 120 125	
ctt ttc cgc tat ggc cac gcg gcc gcc gtg ccc aga aac tgt gga ggt	435
Leu Phe Arg Tyr Gly His Ala Ala Ala Val Pro Arg Asn Cys Gly Gly	
130 135 140	
gat tgc aag cct tgt ata tgt aca ggc tca gaa gta tca tct gtc ttc	483
Asp Cys Lys Pro Cys Ile Cys Thr Gly Ser Glu Val Ser Ser Val Phe	
145 150 155	
atc ttc ccc cca aag ccc aaa gat gtg ctc acc atc act ctg act cct	531
Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro	
160 165 170	
aag gtc acg tgt gtt gtg gta gac att agc cag gac gat ccc gag gtc	579
Lys Val Thr Cys Val Val Val Asp Ile Ser Gln Asp Asp Pro Glu Val	
175 180 185	

cat ttc agc tgg ttt gta gat gac gtg gaa gtc cac aca gct cag act 627
His Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr
190 195 200 205

cga cca cca gag gag cag ttc aac agc act ttc cgc tca gtc agt gaa 675
Arg Pro Pro Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu
210 215 220

ctc ccc atc ctg cac cag gac tgg ctc aat ggc agg acg ttc aga tgc 723
Leu Pro Ile Leu His Gln Asp Trp Leu Asn Gly Arg Thr Phe Arg Cys
225 230 235

aag gtc acc agt gca gct ttc cca tcc ccc atc gag aaa acc atc tcc 771
Lys Val Thr Ser Ala Ala Phe Pro Ser- Pro Ile Glu Lys Thr Ile Ser
240 245 250

aaa ccc gaa ggc aga aca caa gtt ccg cat gta tac acc atg tca cct 819
Lys Pro Glu Gly Arg Thr Gln Val Pro His Val Tyr Thr Met Ser Pro
255 260 265

acc aag gaa gag atg acc cag aat gaa gtc agt atc acc tgc atg gta 867
Thr Lys Glu Glu Met Thr Gln Asn Glu Val Ser Ile Thr Cys Met Val
270 275 280 285

aaa ggc ttc tat ccc cca gac att tat gtg gag tgg cag atg aac ggg 915
Lys Gly Phe Tyr Pro Pro Asp Ile Tyr Val Glu Trp Gln Met Asn Gly
290 295 300

cag cca cag gaa aac tac aag aac act cca cct acg atg gac aca gat 963
Gln Pro Gln Glu Asn Tyr Lys Asn Thr Pro Pro Thr Met Asp Thr Asp
305 310 315

ggg agt tac ttc ctc tac agc aag ctc aat gtg aag aag gaa aaa tgg 1011
Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Asn Val Lys Lys Glu Lys Trp
320 325 330

cag cag gga aac acg ttc acg tgt tct gtg ctg cat gaa ggc ctg cac 1059
Gln Gln Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His

335 340 345

aac cac cat act gag aag agt ctc tcc cac tct ccg ggt aaa gcc caa 1107
Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys Ala Gln

350 355 360 365

gat ttt gtg cag tgg ttg atg aat acc tgagaattc 1143
Asp Phe Val Gln Trp Leu Met Asn Thr

370

<210> 6

<211> 825

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (13)..(816)

<223> DNA insert encoding rat signal peptide, rat IgG Fc region and glucagon C19-29 region

<400> 6

gaattcattt aa atg aag tcc tgc ggc ctg ttc cct ctc atg gtg ctc ctt 51

Met Lys Ser Cys Gly Leu Phe Pro Leu Met Val Leu Leu

1 5 10

gct ctg ggt gta ctg gca ccc tgg agt gtg gaa gga gcg gcc gcc gtg 99

Ala Leu Gly Val Leu Ala Pro Trp Ser Val Glu Gly Ala Ala Ala Val

15 20 25

ccc aga aac tgt gga ggt gat tgc aag cct tgt ata tgt aca ggc tca 147

Pro Arg Asn Cys Gly Gly Asp Cys Lys Pro Cys Ile Cys Thr Gly Ser

30 35 40 45

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gaa gta tca tct gtc ttc atc ttc ccc cca aag ccc aaa gat gtg ctc	195
Glu Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu	
50 55 60	
acc atc act ctg act cct aag gtc acg tgt gtt gtg gta gac att agc	243
Thr Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser	
65 70 75	
cag gac gat ccc gag gtc cat ttc agc tgg ttt gta gat gac gtg gaa	291
Gln Asp Asp Pro Glu Val His Phe Ser Trp Phe Val Asp Asp Val Glu	
80 85 90	
gtc cac aca gct cag act cga cca cca gag gag cag ttc aac agc act	339
Val His Thr Ala Gln Thr Arg Pro Pro Glu Glu Gln Phe Asn Ser Thr	
95 100 105	
ttc cgc tca gtc agt gaa ctc ccc atc ctg cac cag gac tgg ctc aat	387
Phe Arg Ser Val Ser Glu Leu Pro Ile Leu His Gln Asp Trp Leu Asn	
110 115 120 125	
ggc agg acg ttc aga tgc aag gtc acc agt gca gct ttc cca tcc ccc	435
Gly Arg Thr Phe Arg Cys Lys Val Thr Ser Ala Ala Phe Pro Ser Pro	
130 135 140	
atc gag aaa acc atc tcc aaa ccc gaa ggc aga aca caa gtt ccg cat	483
Ile Glu Lys Thr Ile Ser Lys Pro Glu Gly Arg Thr Gln Val Pro His	
145 150 155	
gta tac acc atg tca cct acc aag gaa gag atg acc cag aat gaa gtc	531
Val Tyr Thr Met Ser Pro Thr Lys Glu Glu Met Thr Gln Asn Glu Val	
160 165 170	
agt atc acc tgc atg gta aaa ggc ttc tat ccc cca gac att tat gtg	579
Ser Ile Thr Cys Met Val Lys Gly Phe Tyr Pro Pro Asp Ile Tyr Val	
175 180 185	

18/28

gag tgg cag atg aac ggg cag cca cag gaa aac tac aag aac act cca 627
Glu Trp Gln Met Asn Gly Gln Pro Gln Glu Asn Tyr Lys Asn Thr Pro
190 195 200 205

cct acg atg gac aca gat ggg agt tac ttc ctc tac agc aag ctc aat 675
Pro Thr Met Asp Thr Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Asn
210 215 220

gtg aag aag gaa aaa tgg cag cag gga aac acg ttc acg tgt tot gtg 723
Val Lys Lys Glu Lys Trp Gln Gln Gly Asn Thr Phe Thr Cys Ser Val
225 230 235

ctg cat gaa ggc ctg cac aac cac cat act gag aag agt ctc tcc cac 771
Leu His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His
240 245 250

tct ccg ggt aaa gcc caa gat ttt gtg cag tgg ttg atg aat acc 816
Ser Pro Gly Lys Ala Gln Asp Phe Val Gln Trp Leu Met Asn Thr
255 260 265

tgagaattc 825

<210> 7

<211> 1284

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (13).. (1275)

<223> DNA insert encoding rat IL1 receptor antagonist, rat IgG Fc region and glucagon
C19-29 region

<400> 7

gaattcattt aa atg gaa atc tgc tgg gga ccc tac agt cac cta atc tct 51

19/28

Met Glu Ile Cys Trp Gly Pro Tyr Ser His Leu Ile Ser

1

5

10

ctc ctt ctc atc ctt ctg ttt cat tca gag gca gcc tgc cgc cct tct 99
Leu Leu Leu Ile Leu Leu Phe His Ser Glu Ala Ala Cys Arg Pro Ser
15 20 25

ggg aaa aga ccc tgc aag atg caa gcc ttc aga atc tgg gat act aac 147
Gly Lys Arg Pro Cys Lys Met Gln Ala Phe Arg Ile Trp Asp Thr Asn
30 35 40 45

cag aag acc ttt tac ctg aga aac aac cag ctc att gct ggg tac tta 195
Gln Lys Thr Phe Tyr Leu Arg Asn Asn Gln Leu Ile Ala Gly Tyr Leu
50 55 60

caa gga cca aat atc aaa cta gaa gaa aag ata gac atg gtg cct att 243
Gln Gly Pro Asn Ile Lys Leu Glu Glu Lys Ile Asp Met Val Pro Ile
65 70 75

gac ctt cat agt gtg ttc ttg ggc atc cac ggg ggc aag ctg tgc ctg 291
Asp Leu His Ser Val Phe Leu Gly Ile His Gly Gly Lys Leu Cys Leu
80 85 90

tct tgt gcc aag tct gga gat gat atc aag ctc cag ctg gag gaa gtt 339
Ser Cys Ala Lys Ser Gly Asp Asp Ile Lys Leu Gln Leu Glu Glu Val
95 100 105

aac atc act gat ctg agc aag aac aaa gaa gaa gac aag cgc ttt acc 387
Asn Ile Thr Asp Leu Ser Lys Asn Lys Glu Glu Asp Lys Arg Phe Thr
110 115 120 125

ttc atc cgc tct gag aaa ggc ccc acc acc agc ttt gag tca gct gcc 435
Phe Ile Arg Ser Glu Lys Gly Pro Thr Thr Ser Phe Glu Ser Ala Ala
130 135 140

tgt cca gga tgg ttc ctc tgc aca aca cta gag gct gac cgt cct gtg 483

Cys Pro Gly Trp Phe Leu Cys Thr Thr Leu Glu Ala Asp Arg Pro Val	
145 150 155	
agc ctc acc aac aca ccg gaa gag ccc ctt ata gtc acg aag ttc tac	531
Ser Leu Thr Asn Thr Pro Glu Glu Pro Leu Ile Val Thr Lys Phe Tyr	
160 165 170	
ttc cag gaa gac caa gcg gcc gcc gtg ccc aga aac tgt gga ggt gat	579
Phe Gln Glu Asp Gln Ala Ala Ala Val Pro Arg Asn Cys Gly Gly Asp	
175 180 185	
tgc aag cct tgt ata tgt aca ggc tca gaa gta tca tct gtc ttc atc	627
Cys Lys Pro Cys Ile Cys Thr Gly Ser Glu Val Ser Ser Val Phe Ile	
190 195 200 205	
ttc ccc cca aag ccc aaa gat gtg ctc acc atc act ctg act cct aag	675
Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys	
210 215 220	
gtc acg tgt gtt gtg gta gac att agc cag gac gat ccc gag gtc cat	723
Val Thr Cys Val Val Val Asp Ile Ser Gln Asp Asp Pro Glu Val His	
225 230 235	
ttc agc tgg ttt gta gat gac gtg gaa gtc cac aca gct cag act cga	771
Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Arg	
240 245 250	
cca cca gag gag cag ttc aac agc act ttc cgc tca gtc agt gaa ctc	819
Pro Pro Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu	
255 260 265	
ccc atc ctg cac cag gac tgg ctc aat ggc agg acg ttc aga tgc aag	867
Pro Ile Leu His Gln Asp Trp Leu Asn Gly Arg Thr Phe Arg Cys Lys	
270 275 280 285	
gtc acc agt gca gct ttc cca tcc ccc atc gag aaa acc atc tcc aaa	915

Val Thr Ser Ala Ala Phe Pro Ser Pro Ile Glu Lys Thr Ile Ser Lys
 290 295 300

ccc gaa ggc aga aca caa gtt ccg cat gta tac acc atg tca cct acc 963
 Pro Glu Gly Arg Thr Gln Val Pro His Val Tyr Thr Met Ser Pro Thr
 305 310 315

aag gaa gag atg acc cag aat gaa gtc agt atc acc tgc atg gta aaa 1011
 Lys Glu Glu Met Thr Gln Asn Glu Val Ser Ile Thr Cys Met Val Lys
 320 325 330

ggc ttc tat ccc cca gac att tat gtg gag tgg cag atg aac ggg cag 1059
 Gly Phe Tyr Pro Pro Asp Ile Tyr Val Glu Trp Gln Met Asn Gly Gln
 335 340 345

cca cag gaa aac tac aag aac act cca cct acg atg gac aca gat ggg 1107
 Pro Gln Glu Asn Tyr Lys Asn Thr Pro Pro Thr Met Asp Thr Asp Gly
 350 355 360 365

agt tac ttc ctc tac agc aag ctc aat gtg aag aag gaa aaa tgg cag 1155
 Ser Tyr Phe Leu Tyr Ser Lys Leu Asn Val Lys Lys Glu Lys Trp Gln
 370 375 380

cag gga aac acg ttc acg tgt tct gtg ctg cat gaa ggc ctg cac aac 1203
 Gln Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn
 385 390 395

cac cat act gag aag agt ctc tcc cac tct ccg ggt aaa gcc caa gat 1251
 His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys Ala Gln Asp
 400 405 410

ttt gtg cag tgg ttg atg aat acc tgagaattc 1284
 Phe Val Gln Trp Leu Met Asn Thr
 415 420

<210> 8

<211> 369

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (13).. (360)

<223> DNA insert encoding human IL8 and glucagon C19-29 region

<400> 8

gaattcattt aa atg act tcc aag ctg gcc gtg gct ctc ttg gca gcc ttc 51

Met Thr Ser Lys Leu Ala Val Ala Leu Leu Ala Ala Phe

1

5

10

ctg att tct gca gct ctg tgt gaa ggt gca gtt ttg cca agg agt gct 99

Leu Ile Ser Ala Ala Leu Cys Glu Gly Ala Val Leu Pro Arg Ser Ala

15

20

25

aaa gaa ctt aga tgt cag tgc ata aag aca tac tcc aaa cct ttc cac 147

Lys Glu Leu Arg Cys Gln Cys Ile Lys Thr Tyr Ser Lys Pro Phe His

30

35

40

45

ccc aaa ttt atc aaa gaa ctg aga gtg att gag agt gga cca cac tgc 195

Pro Lys Phe Ile Lys Glu Leu Arg Val Ile Glu Ser Gly Pro His Cys

50

55

60

gcc aac aca gaa att att gta aag ctt tct gat gga aga gag ctc tgt 243

Ala Asn Thr Glu Ile Ile Val Lys Leu Ser Asp Gly Arg Glu Leu Cys

65

70

75

ctg gac ccc aag gaa aac tgg gtg cag agg gtt gtg gag aag ttt ttg 291

Leu Asp Pro Lys Glu Asn Trp Val Gln Arg Val Val Glu Lys Phe Leu

80

85

90

aag agg gct gag aat tca gcg gcc gcc ccg ggt aaa gcc caa gat ttt 339

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Lys Arg Ala Glu Asn Ser Ala Ala Ala Pro Gly Lys Ala Gln Asp Phe

95

100

105

gtg cag tgg ttg atg aat acc tgagaattc

369

Val Gln Trp Leu Met Asn Thr

110

115

<210> 9

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer used for constructing a vector pCAGGS-IgG-glu19-29

<400> 9

gagaattcat ttaaatgaga gcggccgccg tgcccagaaa ctgtg

45

<210> 10

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer used for constructing a vector pCAGGS-IgG-glu19-29

<400> 10

tcaaccactg cacaaaatct tgggctttac ccggagagtg ggagagact

49

<210> 11

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer used for constructing a vector pCAGGS-IgG-glu19-29

<400> 11

gagaattcat ttaaagaga gcggccgcg tgcacagaa ctgtg 45

<210> 12

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer used for constructing a vector pCAGGS-IgG-glu19-29

<400> 12

gagagagaga attctcaggt attcatcaac cactgcacaa aatcttgggc 50

<210> 13

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer used for constructing a vector
pCAGGS-IFN-rR-IgG-glu19-29

<400> 13

gagaattcat ttaaagatt ctgctggtgg toctgatg 38

<210> 14

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer used for constructing a vector
pCAGGS-IFN-rR-IgG-glu19-29

<400> 14

gcagcatcgc ggccgcttct tctctgtcat catggagaaa

40

<210> 15

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer used for constructing a vector
pCAGGS-CTLA4-IgG-glu19-29

<400> 15

gagaattcat ttaaattggct tgtcttgac tccagagg

38

<210> 16

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer used for constructing a vector
pCAGGS-CTLA4-IgG-glu19-29

<400> 16

gcagcatcgc ggccgcgtct gaatctgggc atggttctgg

40

<210> 17

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer used for constructing a vector
pCAGGS-IL13-IgG-glu19-29

<400> 17

gagaattcat ttaaatggca ctctgggtga ctgcagtc

38

<210> 18

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer used for constructing a vector
pCAGGS-IL13-IgG-glu19-29

<400> 18

gcagcatogc ggccgcgtgg ccatagcgga aaagttgctt

40

<210> 19

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer used for constructing a vector
pCAGGS-IL1RA-IgG-glu19-29

<400> 19

gagaattcat ttaaatggaa atctgctggg gaccctac

38

<210> 20

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer used for constructing a vector
pCAGGS-IL1RA-IgG-glu19-29

27/28

<400> 20

gcagcatcgc ggccgcttgg tcttcctgga agtagaactt

40

<210> 21

<211> 62

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer used for constructing a vector pCAGGS-glu19-29

<400> 21

gagaattcat ttaaagaga gcggccgccc cgggtaaagc ccaagatttt gtgcagtggg 60

tg 62

<210> 22

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer used for constructing a vector pCAGGS-glu19-29

<400> 22

gagagagaga attctcaggt attcatcaac cactgcacaa aatcttgggc

50

<210> 23

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer used for constructing a vector pCAGGS-IL8-glu19-29

<400> 23

gagaattcat ttaaagact tocaagctgg ccgtggct

38

<210> 24

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer used for constructing a vector pCAGGS-IL8-glu19-29

<400> 24

gcagcatcgc ggccgctgaa ttctcagccc tcttcaaaaa

40